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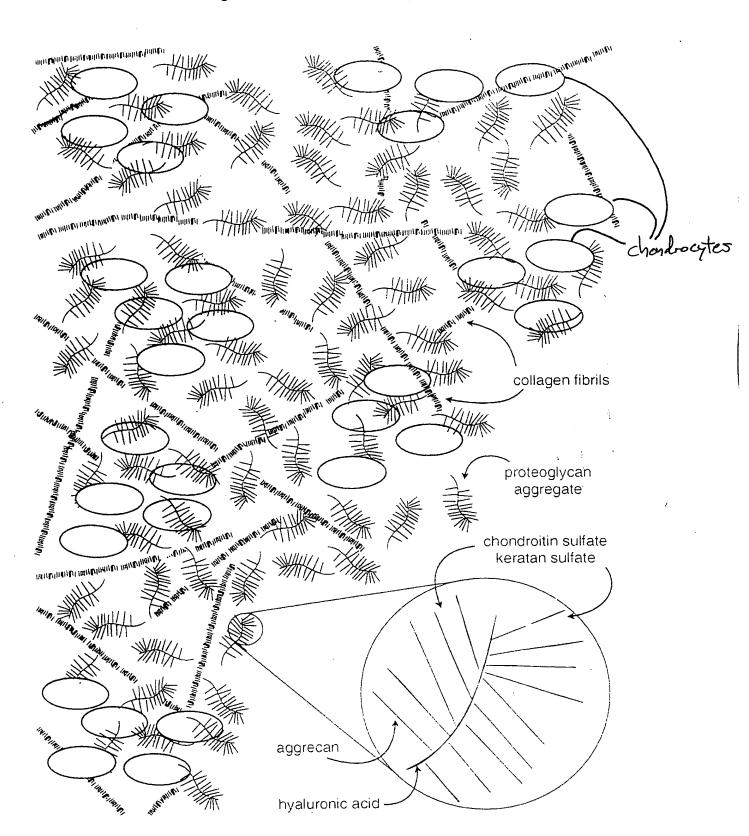
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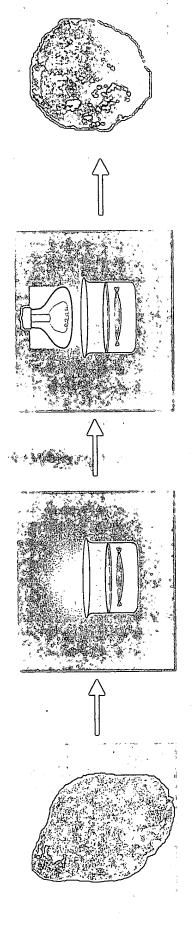
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Figure 1 - Healthy Nucleus Pulposus Tissue



### Cross-linked Mains M.Salle Z.

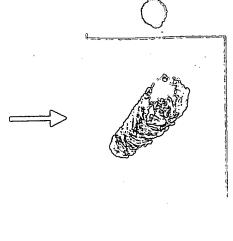


Fresh Porcine Nucleus Pulposus

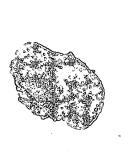
Nucleus Pulposus in HSHS

Photo-catallysed eross-limking

Cross-linked Matrix



Sterille, Lyophillized Cross-linked Matrix

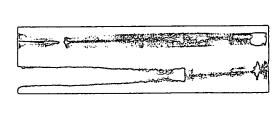


Rehydrated Matrix or

Administer in 22G Syringe

Matrix/BP/serum

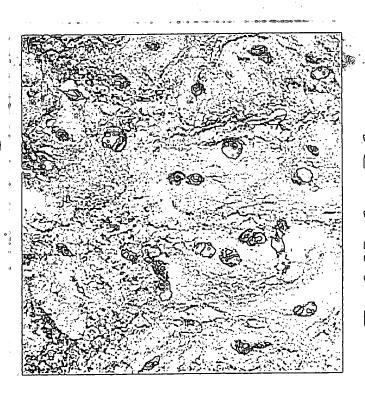
Kigaile 3

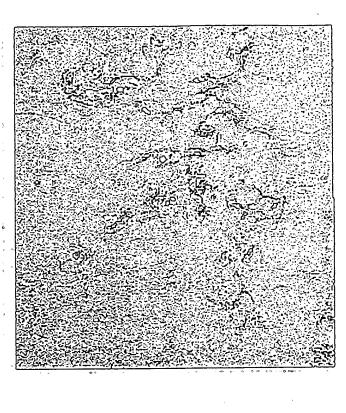


oLane A.: Non cross-linked control shows substantial protein extraction ollame B: Cross-linked matrix démonstrates reduced protein extraction

6

## Nacleus Pulposus versus Cross-linked Matrix Figure 4. Comparison of Kresh Porcine





### Cross-linked Matrix

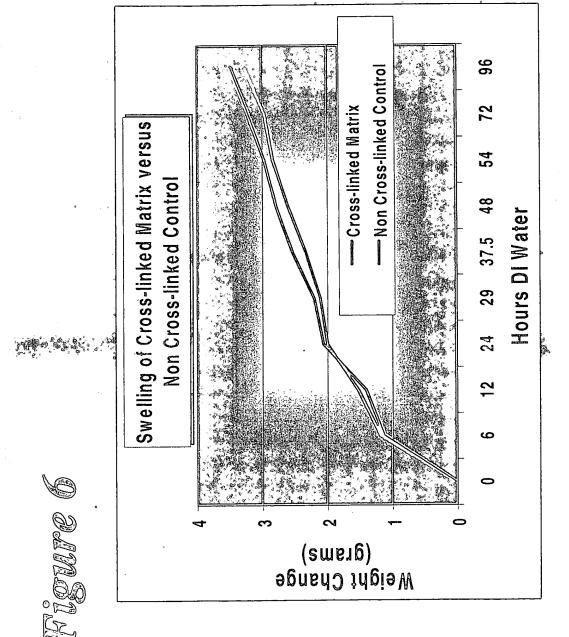
- o dismipted, crenated cell fragments
  - o minimal cell membrane material
    - o further isopropanol sterillization

#### Kigure S



₩ 1B

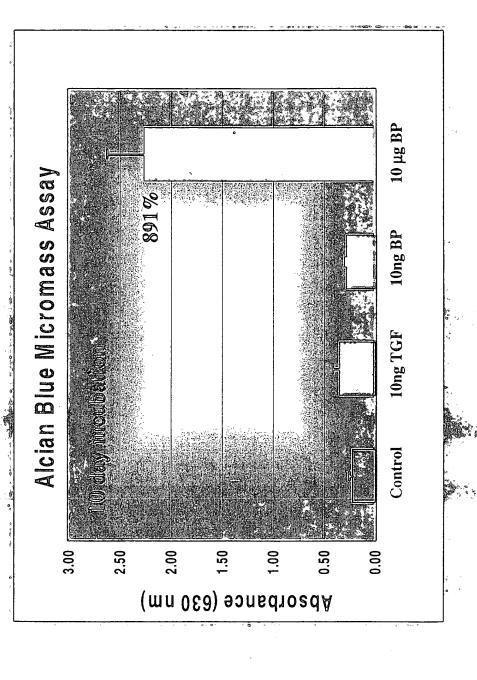
oLame B: Pepsin digests of cross-linked matrix does not react with Type II collagen antibodie olane A.: Pepsin digests of non cross-linked control react with Type II collagen antibodies



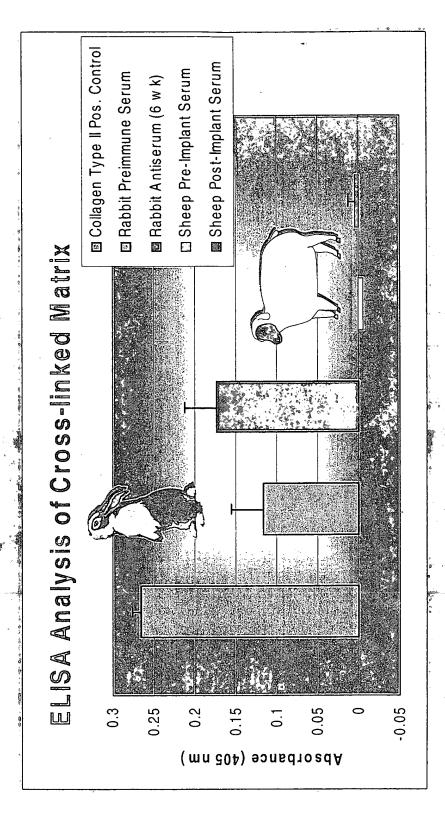
ross-liniked matrix retains 95% hydraulic capaci

#### Cross-limked is skinned with يَ إِنْ طَالَهُ وَهِالَاهُ فَيَ seeded with phalloidin Cross-linked Mainix/BP mathix Disc Cell Culture in Rigure 7: Growth and Proliferation of Disc cells Culture Expansion into Cross-linked Matrix Cross-linked matrix/BP Cell Isolation Sterile nucleus pulposus enzymatic digestion for Cross-linked matrix from sheep spine; cell isolation

# Figure 8: Growth Factor Stimulation of Matrix Synthesis



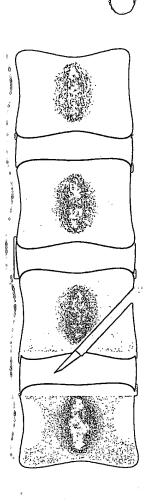
BP concentrations o Signifficant stimulation of mainx production only at ug



Low antilbody titers to cross-linked matrix in rabbit immunizations

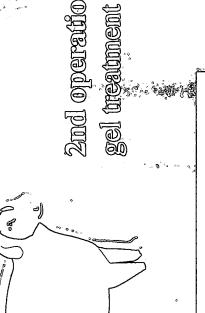
· No serum antilbodies to cross-linked matrix in vivo (1st sheep)

1st operation: annulus stabs to create two degenerative discs

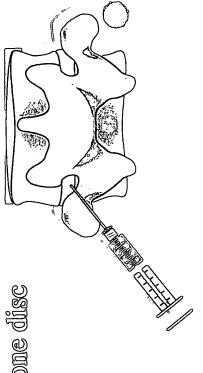


#### Wait 2 months

2nd operation: Cross-linked matrix/BP gel treatment injection to one disc



- · Histomorphometry
- o MIRI/radiographs
- Immune response



Sacriffice: 2, 4, and 6 months

# Figure II. Radiograph-Pilot Study #1 2 Months Post Ingection (Cross-linked matrix/BP)



o Treated and Control discs: Mormal size and appearance of disc structures

o Untreated disc. disjunct endinates, bone resorption and remodelling

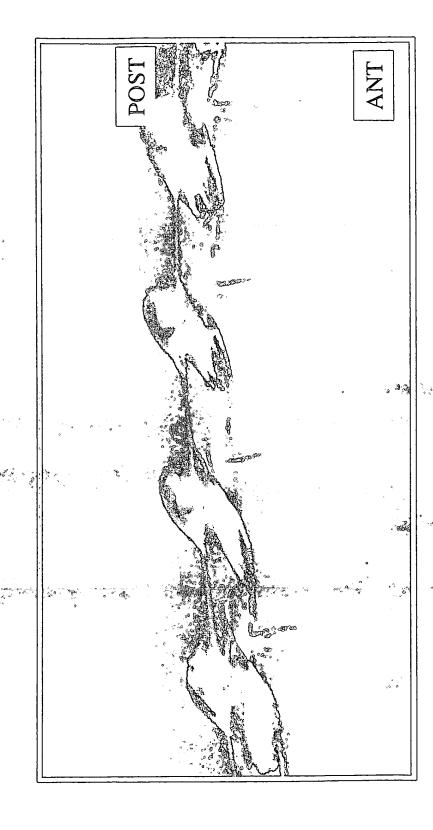
# Figure 12: Histology- Pilot Study #1



## 2 Months Post-Injection

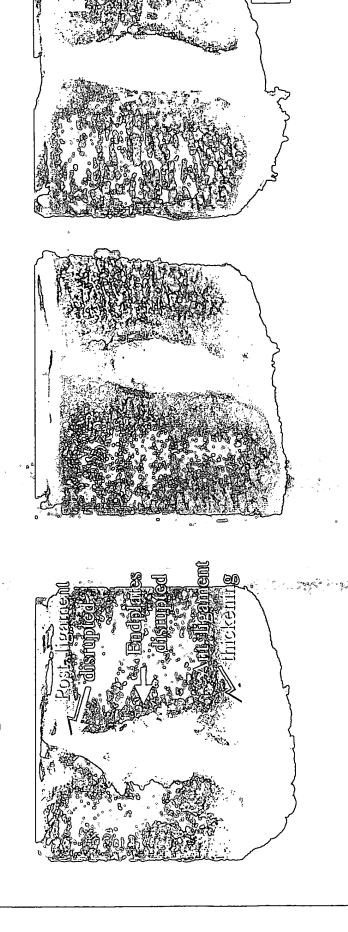
- o Unitreated disc exhilbits extensive degeneration
- o Cross-linked matrix/BP-treated disc retains normal structures similar to Control disc

# Figure 13: Radiograph-Pilot Study #1 4 Months Post Injection (Cross-linked matrix/BP)



o No apparent radiographic differences between discs in 4 month sheep.

# Figure 14: Histology- Pilot Study #1

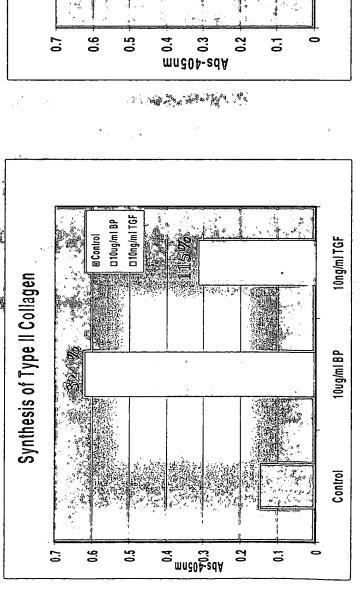


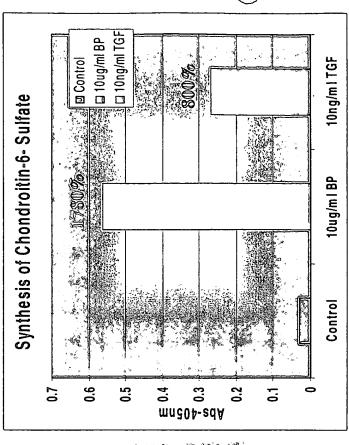
ANT

## 4 Months Post-Injection

- o Untreated disc exhibits degenerative changes
- o Cross-linked matrix/BP-treated disc similar to control disc. normal gelatinous mucleus, regular annulus, intact endiplates

Iype II Collagen & Chondroitin-6-Sulfate Synthesis Figure 15: Crowth Factor Stinudation of

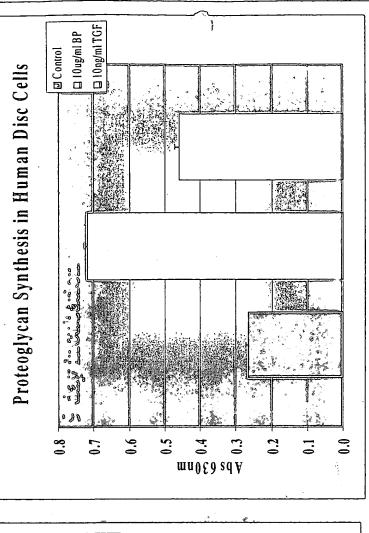


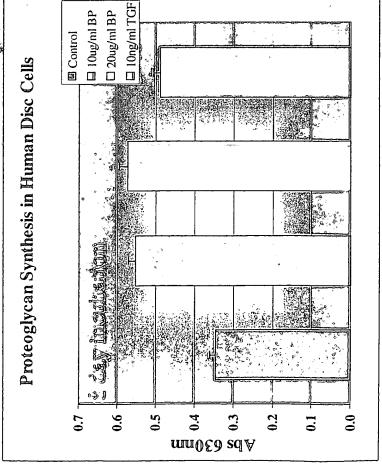


Synthesis in Human Intervertebral Disc Nucleus Pulposus Cells Figure 16: Growth Factor Stimulation of Proteoglycan

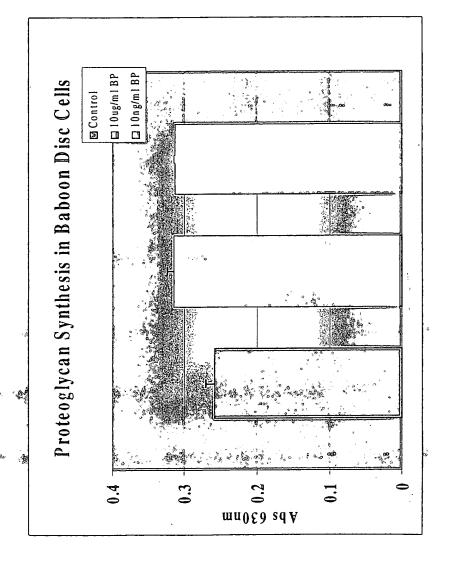
Figure 16a

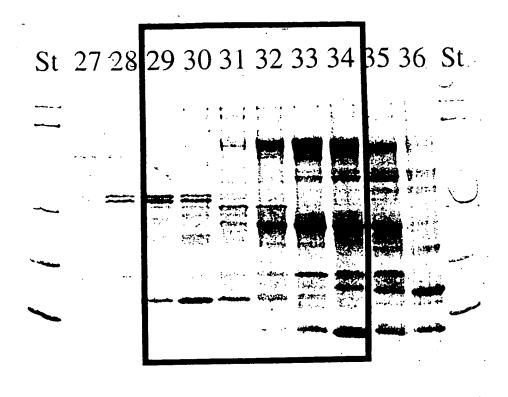


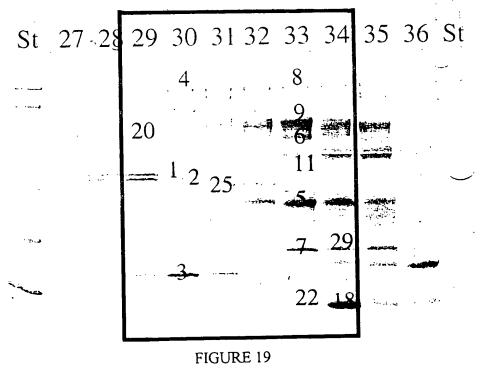




Proteoglycan Synthesis in Baboon Intervertebral Figure II: Growth Factor Stimulation of Disc Nucleus Pulposus Cells







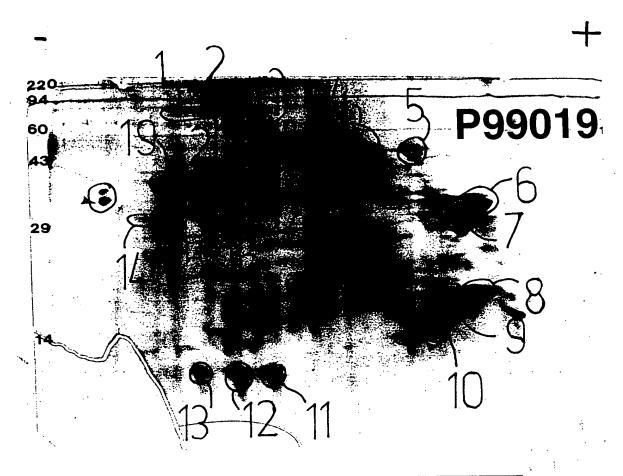
St BP 4/8

Band No.	Identity
1	histone H1.c
2	histone H1.c
3	ribosomal protein RS20
4	similar to ribosomal protein LORP
5	BMP-3
6	α2 macroglobulin RAP & BMP-3
7	similar to ribosomal protein LORP
8	BMP-3
9	BMP-3
11	ribosomal protein RL6 & BMP-3
18	TGF-β2/SPP24
20	Factor H
22	TGF-β2
25	BMP-3 & H1.x
29	BMP-3 & ribosomal protein RL32

FIGURE 20

60 P99019

FIGURE 21



No.	Identity	No.	Identity
l	Factor XIII	11	TGF- β2/SPP24
2	LORP	12	SPP24
3	LORP	12	TGF- β2/SPP24
4		14	lysyl oxidase
5	RL3	15	lysyl oxidase
6		16	lysyl oxidase
7		17	lysyl oxidase
8		18	BMP-3
9		19	cathepsin L
10		20	
		21	RS3a

FIGURE 22

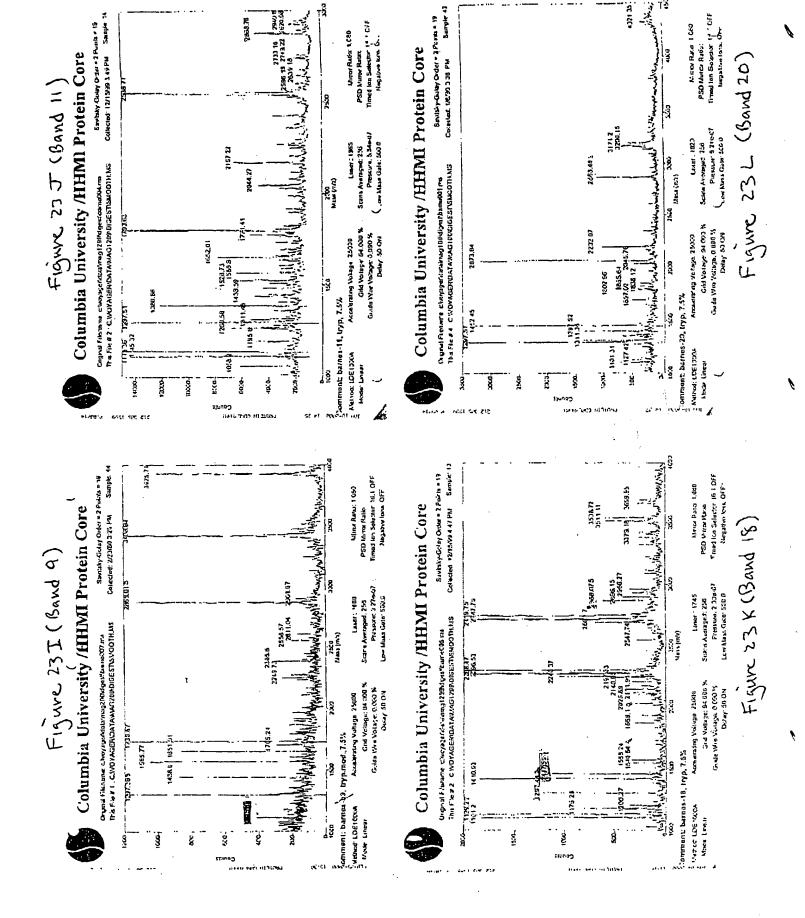
Colected: NA77/199 2:30 P.W. Sumph: 22 Colecad (012/89 2-71Ftd Sample, 75 PSD Mürer Pota Timed Ion Selector, 16.1 Off Negative Ions Off PSO Marce Resor Temal Kn Selgear; 15 1 OFF Negative late, OFF Notice Ratio 1483 Verus Par.a. 1,063 Columbia University /HHMI Protein Core Columbia University /HHMI Protein Core Figure 23 B (Band 2) Stars Astroged 256 Programs 9 Cabult Low Mata Gate: 529 0 Pristar 1584-D6 Mid year Min Luw 1585 Laun: 7955 Scarts Average 1: 236 Ofgnal Fishura: c/uspazzi/czis/naj1099hurasbumc(d).na Fra Fib # i \_ C/USYAGERDATA/IVG(IB999ARNES/9/00FH)IS Organi Flenzne: c'unyagerkalahnagi 0534 gesto pret07.ms Fris File e i : c'hvoyagernaatalangi espidigestishaooth MS Vate (my) 7531 23. ŝ God Vollage 84 CC3 N Gree Voltage: B4,000 % Guda Wre Votaga: 0 075 % Delay: 50 09 Surds VAr Vellage 0.015 % Acceptating Volege. MAN Appriliating Volume 2CCCO 3.341. Somment BARNES-2, trypeln, 7.5 % 16.37 253 ommend: barnes-4, bys 5% 3 Metric LDE 1000A ANTON LDETOXA 7.07 . Š 8 Colorited 10/12/99 2:13 PM Surplet 74 3633, 46, Sampte. 76 PSD Mrias Reio Turad fon Belleton 18.1 Of F Negative fork, Cd f Three lan Subctor, 16-1 OFF Nepstmetons (") Savitaky Galay Onder + 7 Ponts = 19 Savesky-Colay Outer #2 Points # 19 Meror Rates 1 OSSI-Martin Bato 1,060 Columbia University /HHMI Protein Core PS-D former Rates Columbia University /HHIMI Protein Core Colected: 10/12/5/2/3 In PM Scars Averaged 256 Pressues: 1700-16 Prensure 12" bile Figure 23 A. (Band 1) Low Mass Gide; \$400 Starts Averaged 155 THE FIRE LE CONDYAGENDATAMAGIUMDIGESTISMOOTHIMS Crypha Farance c'vopagericatempa (6524) parteamb028 ms Ins. Fig. 9.1. G. v/2VAGEFIDATANING (5590) (655 NSVGOTHANS (4,ta) e1c7 23.03.25 Ond Vatego: 94,093 % Gude Vive Votage: 0.075 % Oesy 50.031 Z4F3.TJ Date: Sel CN Accelerancy Votage, 20530 mentrainy Valley: 76300 . d 15.4 omment BARNES-1, hypsin, 7.5 % Comment BARNES-3, Lypsin, 7.5 % 12,57435 11:32.3 1137 11 Busine UP (1934 Method, LOE 10074 Mode Leads رو. 2 1077 ż ġ XCB. XX 3

Figure 23 D (Band 4

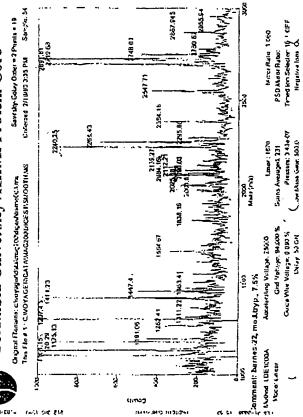
Figure 23C (Band 3)

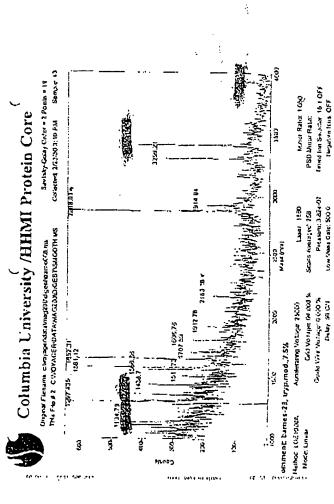
Land

Foredian Sabeton 16 | OFF Colected, 11/1039 3; IB PM Sample F4 Franksian Sylactor 16 i Ciff Nygazina tans: Off Santaky-Gury Order \* 2 Ports \* 19 Name Rada, 1.850 Many Ratio, 1 (50) PED Many Ratio: PSD Mark Ratio 7668.1 344. Columbia University AIHMI Protein Core Culeded, 105.99 1-14 PM Columbia University /HHMI Protein Core Flqure 23H (Band 8) 11, 7, 7, 10,0 Figure 23 F (Band 6) Scons Averejed 256 Pressure 4 014-07 Low JANS Galer 560 0 760145 Pressure: 4.630-07 Laxer 1865 Scars Averaged, 245 Linker, 1895 Odgraf Fignanie e Vrojog ektaleineg Händigerkeiow (Kislins Frit File # 1 - Evuovagerica favland Horomote Ensurooth IVS Onginal Fibrains choyagendalahnagidagiskesthannool.ina Tas Fia a i C.WOYAGEROATAVAGICECIDIGESTISIVCOTHMIS 7000 (311) 4344 (2.m) ese [m/z] Gos Vatage 94,000 & Guse Wild Vallege, 0.075 % Gus Votaça: 94.603 % Duray: 50 GN Guide Wha Voluge: 0.075 % Debyt 40 Ov Accelerating Visions 20043 Acceerating Vorige 2009 1651.69 omment: barnes-3, byp, 7.5% comment: barnes tryps F6 155 32 Method LCE 1032A 250011 COS BREDON LEE I BOOM 8 ξ Ś Later 201 (651 March to the state of the state Collected, 17/10/59 J. 11 PM Survey: 65 FA nor Haber 11980 PGD Natice Haber Trimed Ion Solvetor IF\* CFF 14egative Ions: Ox. . 3575.H Sample, 35 Samaky Gody Order a 2 Porta \* 19 Though his Selector 15 t OFF Hegalize lives, DTF Marica Ratio, 1:063 12/13/49 कर्ड डेम Columbia University /HHMI Protein Core PSD Name Rador emř.3 Columbia University /HHMII Protein Core Caladel, 100559 1 16 PM Figure 23 E (Band 5) Figure 236 (Band 7 Scare Averaged 256
Prevaule 5,66e-07
Com Mess Coty 500 0 2868, N STD. Scars Averaged: 121 / Pressure: 3.69m07 Live Hass Gen 5000 Later, 1935 6861: max Orginal Flansina: etvayayardulumuyi IPAdipadkarow\_Oshina This Fiele 1 ° CIVIDYAGEIRDAI AWAGIISPDAGESTISSIOOTH MS Ongral Flename. Ethograpordalownsylloxidisgenthamsolloms Tyn Fre e 1 - it wydaddenthalaudiosgobkiesthamol HMS 2670 Mises (red) 1753.62 Gred Vorsige" S4 CGG % Gusta Wite Vollage 0.975 % Grivaters of one Accelerating Votage 2000 Guide What Workinger B 875 % Oneay 50 CM Agaztia arreg Volaça: 70000 Comment: Samee-7, tryp, 7.5% " Cit Ct. 16:31 omment: barnes tryps #5 1001 Annea Cot 1000 111332 Mathad LDE:COCA Vede Links Š 47.0



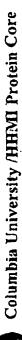
## Columbia University /HHIMI Protein Core





Frywe 23 O (Band 29)

### Figure 23 N (Band 25)



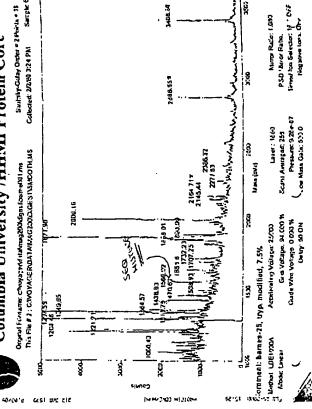
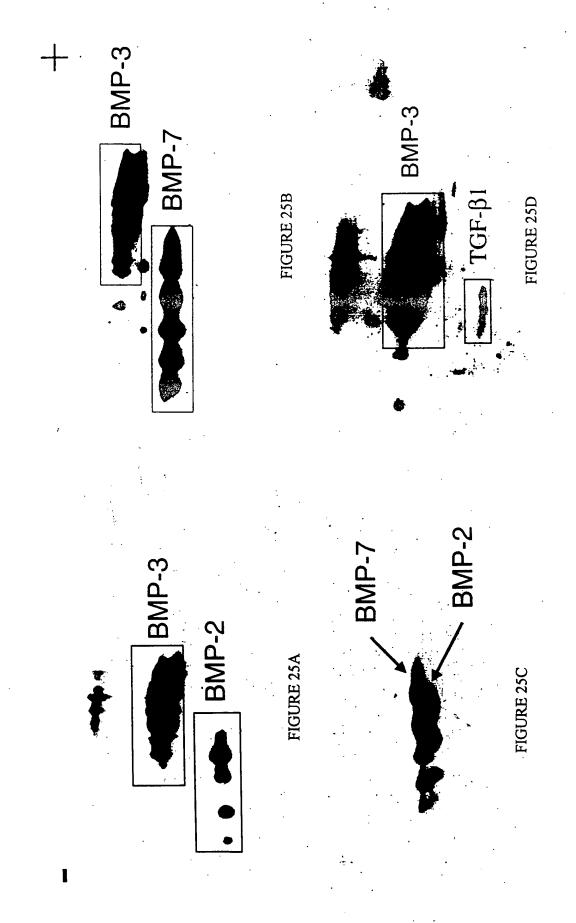
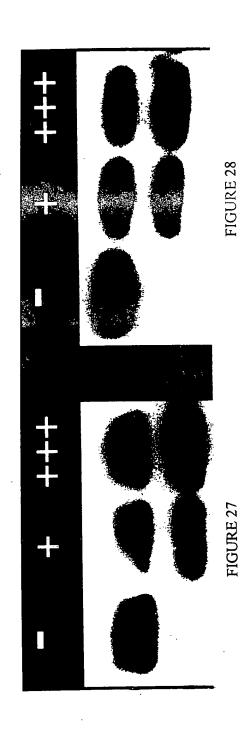
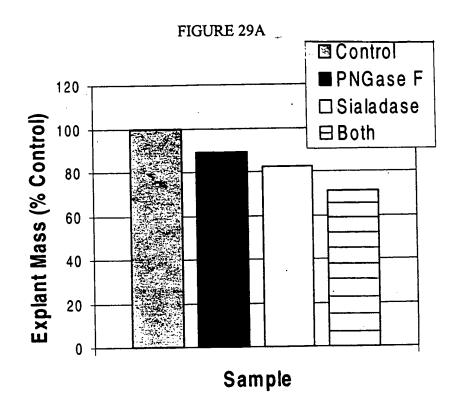


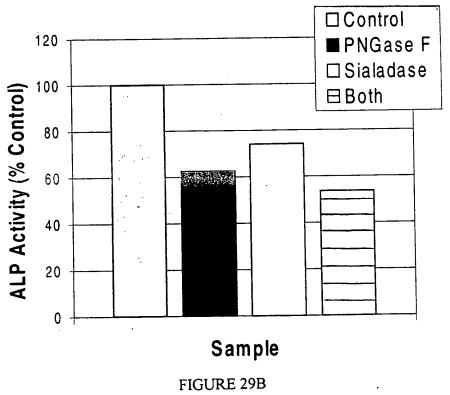
FIGURE 24

2.3









.) FIGURE 30

#### Antibody Information

Specificity	Antigen	Host Species	PC/MC	Source	Catalog No.
TGF-β1 (human)	Protein	Rabbit	Polycional	Promega	G1221
TGF-β2 (human)	Peptide	Rabbit	Polyclonal	Santa Cruz Biotechnology	sc-90
TGF-β3 (human)	Peptide	Rabbit	Polyclonal	Santa Cruz Biotechnology	sc-82
BMP-2 (human)	Protein	Rabbit	Polyclonal	Austral Biologics	PA-513-9
BMP-3 (human)	Peptide	Chicken	Polycional	Research Genetics	NA
BMP-4 (human)	Peptide	Goat	Polycional	Santa Cruz Biotechnology	sc-6896
BMP-5 (human)	Peptide	Goat	Polycional	Santa Cruz Biotechnology	sc-7405
BMP-6 (human)	Peplide	Mouse	Monoclonal	Novocastra Laboratories	NCL-BMP6
BMP-7 (human)	Peptide	Rabbit	Polyclonal	Research Genetics	NA
FGF-1 (human)	Peptide	Goat	Polyclonal	Santa Cruz Biotechnology	sc-1884
osteonectin (bovine)	Protein	Mouse	Monoclonal	DSHB	AON-1
osteocalcin (bovine)	Protein	Rabbit	Polyclonal	Accurate Chemicals	A761/R1H
serum albumin (bovine)	Protein	Rabbit	Polyclonal	Chemicon International	AB870
transferrin (human)	Protein	Chicken	Polyclonal	Chemicon International	AB797
apo-A1 lipoprotein (human)	Protein	Goat	Polycional	Chemicon International	AB740

Figure 31A. Identification of Proteins by Amino Acid Sequencing of Tryptic Fragments

Band	Sample	Sequence Data	Best Database Match Match	_	Identification	Species	Acc. No.	AAs
2	fx 49 (1579)	XLAAAGYDVEK	ALAAAGYDVEK	11/11	histone H1.c	human	87668 (NCBI)	65-75
3	fx 67 (1346)	SLEKVCADLIR	SLEKVCADLIR	11/11	40s Ribosomal Protein S20	rat	R3RT20 (PIR)	31-41
4	fx 65 ()	(V)VCGMLGFPSEAPV	VVCGMLGFPGEKRV 11/14		LORP	mouse	AAC95338 (NCBI)	213- 226
5	N terminal seq	STGVLLPLQNNELPG	STGVLLPLQNNELPG	15/15	BMP-3	human		290- 304
	fx 72 (3925)	STGVLLPLQNNELPGA EYQY	STGVLLPLQNNELPG 20/20 AEYQY		BMP-3	human		290- 309
	fx 74 (3409)	STGVLLPLQ	STGVLLPLQ	6/6	BMP-3	human		290- 298
ဖြ	fx 55 (1566)	(S)QTLQFXE	SQTLQFDE	7/8	BMP-3	human	4557371 (NCBI)	346- 353
	fx 47	VYAF	no match		555			
	N terminal seq	HAGKYSREKNT(P)A(P )	REKNOPKP	11/14	α2-Macroglobulin Receptor Assoc. Pro.	human	P30533 (Swiss-Prot)	31-46
	fx 57 (1438)	SQTLQFDEQ	SQTLQFDEQ	6/6	BMP-3	human	4557371 (NCBI)	346- 354
	fx 57 (1652)	SLKPSNHA	SLKPSNHA	8/8	BMP-3	human		410-
_	fx 51 (1093)	AALRPLVKP	AALRPLVKP	6/6	60s Ribosomal Protein L32	mouse	P17932 (Swiss-Prot)	1-9
	fx 37 (no MS)	A(H)I(Q)VERYV	AIVER	5/5	60s Ribosomal Protein L32	mouse	P17932 (Swiss-Prot)	109- 113
	fx 37 (no MS)	A(H)I(Q)VERYV	н <b>о</b> ѕркүу	5/7	60s Ribosomal Protein L32	mouse	P17932 (Swiss-Prot)	22-28
8	fx 78 ()	XALF(G)AQLGXALGPI	no match		777			
6	fx 56 (1567)	SQTLQFDEQT	SATLAFDEAT	10/10	BMP-3	human	P12645 (Swiss-Prot)	346- 355

Figure 318. Identification of Proteins by Amino Acid Sequencing of Tryptic Fragments

Band	Sample	Seguence Data	Best Database Match Match		Identification	Species	Acc. No.	AAs
=	fx 55	SQTLXF	SQTLQF	9/9	BMP-3	human	4557371	346-
	(1311)						(NCBI)	351
	fx 47	VLATVTKPVGGDK	VLATVTKPVGGDK	13/13	60s Ribosomal Protein L6	human	Q02878	87-99
	(1772)						(Swiss-Prot)	
	fx 76	×VFAL	VFAL	4/4	60s Ribosomal Protein L6	human		273-
	(1795)						(Swiss-Prot)	276
	fx 61	AVPQLQGYLR	AIPQLQGYLR	9/10	60s Ribosomal Protein L6	human	Q02878	262-
	(1145)						(Swiss-Prot)	271
<del>2</del>								
22	fx 58	AI DAAYCFR	ALDAAYCFR	6/6	TGF-82	human	P08112	303-
}	(1101)						(Swiss-Prot)	311
	fx 69 (no	GYNANFCAGACPYL	GYNANFCAGACPYL 14/14	14/14	TGF-82	human	P08112	340-
	match)						(Swiss-Prot)	353
	fx 66	VNSQSLSPY	VNSQSLSPY	6/6	SPP24	bovine	Q27967	42-50
	(1411.71)						(Swiss-Prot)	
25	fx 39	KAAKPSV(P)	KAAKPSVP	8/8	Histone H1.x	human	JC4928 (PIR)	199-
	(1470)							506
<b>5</b> 8								
			American					

fx = fraction number (molecular weight of fragment, as measured by SDS-PAGE)

Figure 32A. Identification of Proteins by Mass Spectrometry of Tryptic Fragments

					Y		- 1		<del></del>		- 1	_	- Y					$\neg$
Comments		15 MS peaks match with Band 2				identification of starred peptide confirmed by sequence analysis		15 MS peaks match with Band 1								12 MS peaks match with Band 8		
% Cover-	age	22				16			62							ω		
AAs		110-121	62-79	64-79	35-54	65-79*	64-79	35-54	50-59	76-83	56-66	88-99	9-21	5-21	88-119	150-167	648-669	455-478
Mass Diff-	erence	09.0	0.16	0.58	-0.74	0.05	0.13	-0.20	0.36	-0.09	-0.16	0.55	0.27	-0.17	-0.85	-0.32	-0.28	0.47
Mass	Spec Database	1172.37	1579.71	1707.89	2012.32	1579.71	1707.89	2012.32	1129.40	1156.30	1334.62	1351.58	1517.77	1919.19	3404.87	1988.27	2410.63	2610.10
Mass	Spec Data	1172.97	1579.87	1708.47	2011.58	1579.76	1708.02	2012.12	1129.76	1156.21	1334.46	1352.13	1518.04	1919.02	3404.02	1987.95	2410.35	2610.57
Acc. No.		87668 (NCBI)				87668 (NCBI)			R3RT20 (PIR)							NP002309 (Swiss- Prot)		
Species		human				human			rat							human		
Mass Spec	Profile	4 peaks match with				3 peaks match with histone H1.c			7 peaks match with ribosome S20							3 peaks match with Lysyl Oxidase RP		
Band		-				2			က							4		

Figure 32B. Identification of Proteins by Mass Spectrometry of Tryptic Fragments

Comments		% coverage calculation is relative to the mature BMP-3, 183 AAS (290-472)						identification of starred peptide confirmed by	sequence analysis					% coverage calculation is relative to the mature BMP-3, 183 AAS (290-472)		
% Cover-	age	48									17			15		
AAs		361-368	346-357	345-357	410-424	346-360	374-392	373-392		290-318*	283-290	129-150	257-282	346-357	410-424	
Mass Diff-	erence	0.01	-0.05	00.00	-0.05	0.07	-0.17	-0.36		1.38	0.09	0.15	-0.01	0.18	-0.03	
Mass	Spec Database	1113.31	1438.58	1566.76	1651.91	1794.02	2268.63	2424.81		3407.77	1002.15	2362.43	3048.52	1566.75	1651.91	
Mass	Spec Data	1113.32	1438.53	1566.76	1651.86	1794.09	2268.46	2424.45		3409.15	1002.24	2362.58	3048.51	1566.93	1651.88	
Acc. No.		4557371 (NCBI)									P30533 (Swiss- Prot)			4557371 (NCBI)		
Species	•	human									human			human		
Mass Spec	Profile	9 peaks match with BMP-3									3 peaks match with α2- Macroglobuli	n KAP		2 peaks match with BMP-3		
Band		2									ထ					

Figure 32 C. Identification of Proteins by Mass Spectrometry of Tryptic Fragments

Г		1		$\neg$	$\neg$							<u>"</u>					$\neg$
Comments						% coverage calculation is relative to the mature BMP-3, 183 AAS (290-472)					12 MS peaks match with Band 4	% coverage calculation is relative to the mature BMP-3, 183 AAS (290-472)					
% Cover-	age	. 33				21					£ .	36					
AAs		67-75	1-10*	65-74	19-29	102-111	361-368	190-200	410-424	346-360	648-669	361-368	346-357	345-357	410-424	41-66	290-318
Mass Diff-	erence	0.08	60.0-	0.44	0.12	0.22	0.08	-0.32	0.37	-0.40	-0.26	-0.17	0.02	0.01	0:30	0.48	1.17
Mass	Spec Database	1033.17	1093.40	1134.28	1449.66	1060.20	1113.31	1360.58	1651.91	1794.02	2410.63	1113.31	1438.58	1566.76	1651.61	2901.19	3407.77
Mass	Spec Data	1033.25	1093.31	1134.72	1449.78	1060.42	1113.39	1360.26	1652.28	1793.62	2410.37	1113.14	1438.60	1566.77	1651.91	2901.67	3408.94
Acc. No.		P17932 (Swiss- Prot)				4557371 (NCBI)					NP002309 (Swiss- Prot)	4557371 (NCBI)					
Species		mouse				human					human	human					
Mass Spec	Profile	4 peaks match with ribosome L32				5 peaks match with BMP-3					1 peak matches with Lysyl Oxidase RP	6 peaks match with BMP-3					
Band		7				•					ω	<b>o</b>					

Figure 32 D. Identification of Proteins by Mass Spectrometry of Tryptic Fragments

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Comments		% coverage calculation is relative to the mature BMP-3, 183 AAS (290-472)																		
% Cover-	age	48					16					52				30				
AAs		361-368	410-424	346-360	373-392	290-318	114-122	141-155	10-20	262-271	260-271	303-311	400-409	312-328	340-362	42-53	113-124	86-98	62-77	33-53
Mass Diff-	erence	-0.08	-0.18	-0.44	-0.57	0.57	0.15	0.02	0.03	0.01	90.0	90:0-	-0.16	-0.23	-0.21	-0.67	-0.06	0.04	0.05	-0.10
Mass	Spec Database	1113.31	1651.91	1794.02	2424.81	3407.77	1140.23	1526.86	1059.12	1145.35	1386.68	1101.26	1175.42	2240.60	2691.91	1411.60	1447.65	1540.60	1869.05	2268.57
Mass	Spec Data	1113.23	1651.73	1793.58	2424.24	3408.34	1140.38	1526.88	1059.15	1145.36	1386.74	1101.20	1175.26	2240.37	2691.70	1410.93	1447.59	1540.64	1869.10	2268.47
Acc. No.		4557371 (NCBI)					Q02878 (Swiss- Prot)		P47911 (Swiss- Prot)	)		P08112 (Swiss- Prot)	•			Q27967 (Swiss- Prot)			•	
Species		human		•			human		esnom			human				bovine				
Mass Spec	Profile	5 peaks match with BMP-3	,				5 peaks match with ribosome L6					4 peaks match with TGF-82				5 peaks match with SPP24				
Band		<del></del>										18								

Figure 32 E. Identification of Proteins by Mass Spectrometry of Tryptic Fragments

									25									22			Band
				5 peaks match with BMP-3			,		5 peaks match with histone H1.x		match with SPP24	2 peaks					match with TGF-β2	5 peaks		Profile	Mass Spec
				human					human		-	bovine						human			Species
				(NCBI)					JC4928 (PIR)		(Swiss- Prot)	Q27967		•		-	(SWISS- Prot)	P08112			Acc. No.
3408.86	1651.80	1566.92	1438.83	1060.43	1732.23	1364.57	1349.85	1221.71	1208.46	1447.40		1411.23	2691.61	2240.25	2084.16	1175.13		1101.15	Data	Spec	Mass
3407.77	1651.91	1566.76	1438.58	1060.20	1732.97	1364.59	1350.52	1222.35	1208.40	1447.65		1411.60	2691.91	2240.60	2084.42	1175.42		1101.26	Database	Spec	Mass
1.09	-0.11	0.16	0.25	0.23	-0.74	-0.02	-0.67	-0.64	0.06	-0.25		-0.37	-0.30	-0.35	-0.26	-0.29		-0.11		erence	-Mass Diff-
290-318	410-424	345-357	346-357	102-111	43-57	48-58	107-119	107-118	48-57	113-124		42-53	340-362	312-328	312-347	400-409		303-311			AAs
				3					<u>-1</u> 4			11						ნა		age	% Cover-
				% coverage calculation is relative to the mature BMP-3, 183 AAS (290-472)								,									Comments

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Figure 32F. Identification of Proteins by Mass Spectrometry of Tryptic Fragments

		290-318	1.27	3409.04 3407.77	3409.04				
		345-357	0.11	1566.75	1566.86				
		346-357	0.12	1438.58	1438.70			,	
3, 183 AAS (290-472)								BMP-3	
relative to the mature BMP-					-	(NCBI)		match with	
% coverage calculation is	27	361-368	-0.09	1113.31	1113.22	4557371	human	4 peaks	29
				Database	Data			•	
	age		erence	Spec	Spec			Profile	-
Comments	% Cover-	AAs	Mass Diff-	Mass	Mass	Acc. No.	Species	Mass Spec	Band

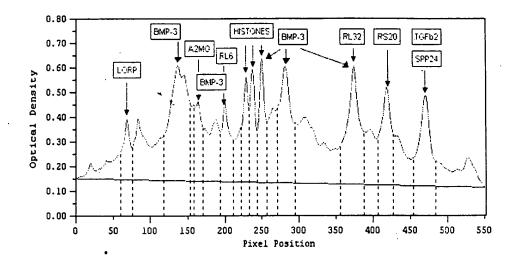


FIGURE 33A



FIGURE 33B

Figure 34. Quantitation of Identified BP proteins

Identified Protein	Percentage of Total Protein
LORP	2
BMP-3	11
BMPO3 & A2-MG	3
RL6 & BMP-3	4
Histone	3
Histone	3
Histone & BMP-3	4
BMP-3	8
RL32 & BMP-3	8
RS20	5
SPP24 & TGF-β2	6
Total	58%